

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SmithKline Beecham, Corporation
- (ii) TITLE OF INVENTION: Recombinant Feline Coronavirus S Proteins
- (iii) NUMBER OF SEQUENCES: 54
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SmithKline Beecham Corporation
 - (B) STREET: 709 Swedeland Road
 - (C) CITY: King of Prussia
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19406-2799
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/698,927
 - (B) FILING DATE: 13-MAY-1991
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/613,066
 - (B) FILING DATE: 14-NOV-1990
- (ix) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: King, William T.
 - (B) REGISTRATION NUMBER: 30,954
 - (C) REFERENCE/DOCKET NUMBER: SBC 14532B
- (x) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (215) 270-5015
 - (B) TELEFAX: (215) 270-5090

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGCCCCCGG GTATGATTGT GCTCGTAAC TGCCTCTTG

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAATAACCCGG GCACGTGAA TGCACGTGGT AAACC

35

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTATTCCCGG GCACGCTCAA GCACGTGCTAC CTGGG

35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGATCCCGG GGTACAATCT GGTATGGGTG CTACAG

36

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTTACCCGG GGTGGTTATG GTCAACCCAT AGCCTCGAC

39

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGTGACCCGG GCGCCATGTG ATGTAAGCGC ACAAGCGGC

39

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCAATCCCGG GGGGTGCCAG ACTTGAAAAC ATGGAGG

37

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTACCCGG GGGTGCCTT GGTGGTGGCG CCGTGGC

37

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAGGTCCCGG GCTCAGTCTC AGAGATTGG ATTCTGTGG

39

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATAATAGGCC TGGTTACCA CGTGCATTAC CAGTGC

36

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTATTAGGCC TCCCAGGTAG CAGTGCTTGA GCGTG

35

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAATAAGGCC TCTGTAGCAC CCATACCAAGA TTGTAC

36

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTAGTAGGCC TGTGAGGCT ATGGGTTGAC CATAACCAC

39

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAACAAGGCC TGCCGTTGT GCGCTTACAT CACATGGCG

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATCAAAGGCC TCCTCCATGT TTTCAAGTCT GGCACCC

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTATAAGGCC TGCCACGGCG CCACCAACAA GTGCACC

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CATTAAGGCC TCCACAGAAT CCGAATCTCT GAGACTGAG

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TAAATAGGCC TTTAGTGGAC ATGCACTTT TCAATTGG

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | |
|---|-----|
| ATG GAT CCC GAA TTC CAA GAA AAA ACA CAA TCT CTG TTT GCC AAC GCA | 48 |
| Met Asp Pro Glu Phe Glu Lys Thr Gln Ser Leu Phe Ala Asn Ala | |
| 1 5 10 15 | |
| TTT GGC TAC CCT GCC ACT CAC ACC ATT CAG GGC CCT GGC CGC GTG AAT | 96 |
| Phe Gly Tyr Pro Ala Thr His Thr Ile Gln Gly Pro Gly Arg Val Asn | |
| 20 25 30 | |
| TTG ATT GGT GAA CAC ACC GAC TAC AAC GAC GGT TTC GTT CTG CCC TGC | 144 |
| Leu Ile Gly Glu His Thr Asp Tyr Asn Asp Gly Phe Val Leu Pro Cys | |
| 35 40 45 | |
| GCG ATT GAT TAT CAA ACC GTG ATC CCT AAT ACC CGG GGC ACT GGT AAT | 192 |
| Ala Ile Asp Tyr Gln Thr Val Ile Pro Asn Thr Arg Gly Thr Gly Asn | |
| 50 55 60 | |
| GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG CCT GTT AGT | 240 |
| Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val Ser | |
| 65 70 75 80 | |
| GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA CAA AGG CCC | 288 |
| Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg Pro | |
| 85 90 95 | |
| CTT TTA AAA CAT GGG TTA GTG TGT ATA ACT AAA AAT CGC CAT ATT AAC | 336 |
| Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile Asn | |
| 100 105 110 | |
| TAT GAA CAA TTC GCC TCC AAC CAG TGG AAT TCC ACA TGT ACG GGT GCT | 384 |
| Tyr Glu Gln Phe Ala Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly Ala | |
| 115 120 125 | |
| GAC AGA AAA ATT CCC TTC TCT GTC ATA CCC ACG GAC AAT GGA ACA AAA | 432 |
| Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr Lys | |
| 130 135 140 | |
| ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT TAT ATT AGT | 480 |
| Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile Ser | |
| 145 150 155 160 | |
| GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT AAC AAT GTC | 528 |
| Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn Val | |
| 165 170 175 | |
| ACA CTT TTG TAT TCA CGC AGC AGC ACT GCT ACC TGG GAG GCC | 570 |
| Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu Ala | |
| 180 185 190 | |
| TAG | 573 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Asp Pro Glu Phe Gln Glu Lys Thr Gln Ser Leu Phe Ala Asn Ala
 1 5 10 15

Phe Gly Tyr Pro Ala Thr His Thr Ile Gln Gly Pro Gly Arg Val Asn
 20 25 30

Leu Ile Gly Glu His Thr Asp Tyr Asn Asp Gly Phe Val Leu Pro Cys
 35 40 45

Ala Ile Asp Tyr Gln Thr Val Ile Pro Asn Thr Arg Gly Thr Gly Asn
 50 55 60

Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val Ser
 65 70 75 80

Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg Pro
 85 90 95

Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile Asn
 100 105 110

Tyr Glu Gln Phe Ala Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly Ala
 115 120 125

Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr Lys
 130 135 140

Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile Ser
 145 150 155 160

Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn Val
 165 170 175

Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu Ala
 180 185 190

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..4362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | |
|---|-----|
| ATG ATT GTG CTC GTA ACT TGC CTC TTG TTA TGT TCA TAC CAC ACA | 48 |
| Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr | |
| 1 5 10 15 | |
| GTT TTG AGT ACA ACA AAT AAT GAA TGC ATA CAA GTT AAC GTA ACA CAA | 96 |
| Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln | |
| 20 25 30 | |
| TTG GCT GGC AAT GAA AAC CTT ATC AGA GAT TTT CTG TTT AGT AAC TTT | 144 |
| Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe | |
| 35 40 45 | |
| AAA GAA GAA GGA AGT GTA GTT GGT GGT TAT TAC CCT ACA GAG GTG | 192 |
| Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val | |
| 50 55 60 | |
| TGG TAC AAC TGC TCT AGA ACA GCA CAA ACT ACT GCC TTT CAG TAT TTT | 240 |
| Trp Tyr Asn Cys Ser Arg Thr Ala Gln Thr Ala Phe Gln Tyr Phe | |
| 65 70 75 80 | |
| AAT AAT ATA CAT GCC TTT TAT TTT GTT ATG GAA GCC ATG GAA AAT AGC | 288 |
| Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser | |
| 85 90 95 | |
| ACT GGT AAT GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG | 336 |
| Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu | |
| 100 105 110 | |
| CCT GTT AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA | 384 |
| Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln | |
| 115 120 125 | |
| CAA AGG CCC CTT TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC | 432 |
| Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg | |
| 130 135 140 | |
| CAT ATT AAC TAT GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT | 480 |
| His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys | |
| 145 150 155 160 | |
| ACG GGT GCT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT | 528 |
| Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn | |
| 165 170 175 | |
| GGA ACA AAA ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT | 576 |
| Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala | |
| 180 185 190 | |
| TAT ATT AGT GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT | 624 |
| Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe | |
| 195 200 205 | |
| AAC AAT GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GAA | 672 |
| Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu | |
| 210 215 220 | |
| TAC AGT GCT GCA TAT GCT TAC CAA GGT GTT TCT AAC TTC ACT TAT TAC | 720 |
| Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr | |
| 225 230 235 240 | |
| AAG TTA AAT AAC ACC AAT GGT CTA AAA ACC TAT GAA TTA TGT GAA GAT | 768 |
| Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp | |
| 245 250 255 | |

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|---|------|
| TAT GAA CAT TGC ACT GGC TAT GCT ACC AAT GTA TTT GCT CCG ACA TCA Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser 260 265 270 | 816 |
| GGT GGT TAC ATA CCT GAT GGA TTT AGT TTT AAC AAT TGG TTC TTG CTT Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu 275 280 285 | 864 |
| ACA AAT AGT TCC ACT TTT GTT AGT GGC AGG TTT GTA ACA AAT CAA CCA Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro 290 295 300 | 912 |
| TTA TTG ATT AAT TGC TTG TGG CCA GTG CCC AGT TTT GGT GTA GCA GCA Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala 305 310 315 320 | 960 |
| CAA GAA TTT TGT TTT GAA GGT GCA CAG TTT AGC CAA TGT AAT GGT GTG Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val 325 330 335 | 1008 |
| TCT TTA AAT AAC ACA GTG GAT GTT ATT AGA TTC AAC CTT AAT TTC ACT Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr 340 345 350 | 1056 |
| GCA GAT GTA CAA TCT GGT ATG GGT GCT ACA GTA TTT TCA CTG AAT ACA Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr 355 360 365 | 1104 |
| ACA GGT GGT GTC ATT CTT GAA ATT TCA TGT TAT AGT GAC ACA GTG AGT Thr Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser 370 375 380 | 1152 |
| GAG TCT AGT TCT TAC AGT TAT GGT GAA ATC CCG TTC GGC ATA ACT GAC Glu Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp 385 390 395 400 | 1200 |
| GGA CCA CGA TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAA TAT Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr 405 410 415 | 1248 |
| TTA GGA ACA TTA CCA CCC AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp 420 425 430 | 1296 |
| GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445 | 1344 |
| GGT TGT ATA TCT TTT AAT TTA ACC ACT GGT GCT AGT GGA GCT TTT TGG Gly Cys Ile Ser Phe Asn Leu Thr Thr Gly Ala Ser Gly Ala Phe Trp 450 455 460 | 1392 |
| ACA ATT GCT TAC ACA TCG TAT ACT GAA GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480 | 1440 |
| ACA GCT ATT AAA AAT GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495 | 1488 |
| AAA TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510 | 1536 |
| GCT TCA AGT GAA GTA GGT TTC GTT AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525 | 1584 |

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|---|------|
| AGC TTT TTC ACA CAC ACC GCT GTC AAT ATA ACC ATT GAT CTT GGT ATG Ser Phe Phe Thr His Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met 530 535 540 | 1632 |
| AAG CTT AGT GGT TAT GGT CAA CCC ATA GCC TCG ACA CTA AGT AAC ATC Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560 | 1680 |
| ACA CTA CCA ATG CAG GAT AAC AAT ACT GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575 | 1728 |
| AAC CAA TTC TCA GTT TAT GTT CCT TCC ACT TGC AAA AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val Pro Ser Thr Cys Lys Ser Ser Leu Trp 580 585 590 | 1776 |
| GAC AAT ATT TTT AAT CAA GAC TGC ACG GAT GTT TTA GAG GCT ACA GCT Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala 595 600 605 | 1824 |
| GTT ATA AAA ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn 610 615 620 | 1872 |
| TAC TTG ACT TTT AAC AAG TTC TGT TTG TCG TTG AGT CCT GTT GGT GCT Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640 | 1920 |
| AAT TGC AAG TTT GAT GTT GCT GCA CGT ACA AGA ACC AAT GAG CAG GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655 | 1968 |
| GTT AGA AGT CTA TAT GTA ATA TAT GAA GAA GGA GAC AAC ATA GTG GGT Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670 | 2016 |
| GTA CCG TCT GAT AAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asn Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685 | 2064 |
| GAC TCC TGT ACA GAT TAC AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700 | 2112 |
| ATT AGA CGA ACT AAC AGT ACG CTA CTT AGT GGC TTA TAT TAC ACA TCA Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser 705 710 715 720 | 2160 |
| CTA TCA GGT GAT TTG TTA GGC TTT AAA AAT GTT AGT GAT GGT GTC ATT Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile 725 730 735 | 2208 |
| TAT TCT GTG ACG CCA TGT GAT GTA AGC GCA CAA GCG GCT GTT ATT GAT Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp 740 745 750 | 2256 |
| GGT GCC ATA GTT GGA GCT ATG ACT TCC ATT AAC AGT GAA CTG TTA GGT Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly 755 760 765 | 2304 |
| CTA ACA CAT TGG ACA ACG ACA CCT AAT TTT TAT TAC TAC TCT ATA TAT Leu Thr His Trp Thr Thr Pro Asn Phe Tyr Tyr Tyr Ser Ile Tyr 770 775 780 | 2352 |
| AAT TAC ACA AGT GAG AGG ACT CGT GGC ACT GCA ATT GAC AGT AAC GAT Asn Tyr Thr Ser Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp 785 790 795 800 | 2400 |

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|---|------|
| GTT GAT TGT GAA CCT GTC ATA ACC TAT TCT AAT ATA GGT GTT TGT AAA Val Asp Cys Glu Pro Val Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys 805 810 815 | 2448 |
| AAT GGT GCT TTG GTT TTT ATT AAC GTC ACA CAT TCT GAC GGA GAC GTG Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val 820 825 830 | 2496 |
| CAA CCA ATT AGC ACT GGT AAT GTC ACG ATA CCT ACA AAT TTT ACC ATA Gln Pro Ile Ser Thr Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile 835 840 845 | 2544 |
| TCT GTG CAA GTT GAA TAC ATG CAG GTT TAC ACT ACA CCA GTA TCA ATA Ser Val Gln Val Glu Tyr Met Gln Val Tyr Thr Pro Val Ser Ile 850 855 860 | 2592 |
| GAT TGT GCA AGA TAC GTT TGT AAT GGT AAC CCT AGA TGT AAC AAA TTG Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu 865 870 875 880 | 2640 |
| TTA ACA CAA TAT GTG TCT GCA TGT CAA ACT ATT GAA CAA GCA CTT GCA Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala 885 890 895 | 2688 |
| ATG GGT GCC AGA CTT GAA AAC ATG GAG GTT GAT TCC ATG TTG TTT GTC Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val 900 905 910 | 2736 |
| TCG GAA AAT GCC CTT AAA TTG GCA TCT GTT GAG GCG TTC AAT AGT ACA Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr 915 920 925 | 2784 |
| GAA AAT TTA GAT CCT ATT TAC AAA GAA TGG CCT AGC ATA GGT GGT TCT Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Ser Ile Gly Gly Ser 930 935 940 | 2832 |
| TGG CTA GGA GGT CTA AAA GAT ATA CTA CCG TCC CAT AAT AGC AAA CGT Trp Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg 945 950 955 960 | 2880 |
| AAG TAT GGT TCT GCT ATA GAA GAT TTG CTT TTT GAT AAA GTT GTA ACA Lys Tyr Gly Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr 965 970 975 | 2928 |
| TCT GGT TTA GGT ACA GTT GAT GAA GAT TAT AAA CGT TGT ACT GGT GGT Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly 980 985 990 | 2976 |
| TAC GAC ATA GCA GAC TTG GTG TGT GCT CAA TAT TAC AAT GGC ATC ATG Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met 995 1000 1005 | 3024 |
| GTT CTA CCA GGT GTA GCT AAT GCT GAC AAG ATG ACT ATG TAC ACA GCA Val Leu Pro Gly Val Ala Asn Ala Asp Lys Met Thr Met Tyr Thr Ala 1010 1015 1020 | 3072 |
| TCA CTT GCA GGT GGT ATA ACA TTA GGT GCA CTT GGT GGT GGC GCC GTG Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Gly Ala Val 1025 1030 1035 1040 | 3120 |
| GCT ATA CCT TTT GCA GTA GCA GTC CAG GCT AGA CTT AAT TAT GTT GCT Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala 1045 1050 1055 | 3168 |
| CTA CAA ACT GAT GTA TTG AAT AAA AAC CAA CAG ATC CTG GCT AAT GCT Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala 1060 1065 1070 | 3216 |

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| TTC AAT CAA GCT ATT GGT AAC ATT ACA CAG GCT TTT GGT AAG GTT AAT Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn 1075 1080 1085 | 3264 |
| GAT GCT ATA CAT CAA ACA TCA CAA GGT CTT GCC ACT GTT GCT AAA GCG Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala Thr Val Ala Lys Ala 1090 1095 1100 | 3312 |
| TTG GCA AAA GTG CAA GAT GTT GTC AAC ACA CAA GGG CAA GCT TTA AGT Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser 1105 1110 1115 1120 | 3360 |
| CAC CTT ACA GTA CAA TTG CAA AAT AAT TTT CAA GCC ATT AGT AGT TCT His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser 1125 1130 1135 | 3408 |
| ATT AGT GAT ATT TAT AAC AGG CTT GAC GAA CTG AGT GCT GAT GCA CAA Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln 1140 1145 1150 | 3456 |
| GTT GAT AGG CTG ATT ACA GGT AGA CTT ACA GCA CTT AAT GCA TTT GTG Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val 1155 1160 1165 | 3504 |
| TCT CAG ACT CTA ACC AGA CAA GCA GAG GTT AGG GCT AGT AGA CAA CTT Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu 1170 1175 1180 | 3552 |
| GCC AAA GAC AAG GTT AAT GAA TGT GTT AGG TCT CAG TCT CAG AGA TTC Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe 1185 1190 1195 1200 | 3600 |
| GGA TTC TGT GGT AAT GGT ACA CAT TTG TTT TCA CTA GCA AAT GCA GCA Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala 1205 1210 1215 | 3648 |
| CCA AAT GGC ATG ATT TTC TTT CAT ACA GTA CTA TTA CCA ACA GCT TAT Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr 1220 1225 1230 | 3696 |
| GAA ACT GTA ACA GCT TGG TCA GGT ATT TGT GCT TCA GAT GGC GAT CGC Glu Thr Val Thr Ala Trp Ser Gly Ile Cys Ala Ser Asp Gly Asp Arg 1235 1240 1245 | 3744 |
| ACT TTC GGA CTT GTC GTT AAA GAT GTG CAG TTG ACG TTG TTT CGT AAT Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn 1250 1255 1260 | 3792 |
| CTA GAT GAC AAG TTC TAT TTG ACC CCC AGA ACT ATG TAT CAG CCT AGA Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg 1265 1270 1275 1280 | 3840 |
| GTT GCA ACT AGT TCT GAT TTT GTT CAA ATT GAA GGG TGT GAT GTG TTG Val Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu 1285 1290 1295 | 3888 |
| TTT GTC AAC GCG ACT GTA ATT GAT TTG CCT AGT ATT ATA CCT GAC TAT Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr 1300 1305 1310 | 3936 |
| ATT GAC ATT AAT CAA ACT GTT CAA GAC ATA TTA GAA AAT TAC AGA CCA Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro 1315 1320 1325 | 3984 |
| AAC TGG ACT GTA CCT GAA TTT ACA CTT GAT ATT TTC AAC GCA ACC TAT Asn Trp Thr Val Pro Glu Phe Thr Leu Asp Ile Phe Asn Ala Thr Tyr 1330 1335 1340 | 4032 |

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| TTA AAT CTG ACT GGT GAA ATT GAT GAC TTA GAG TTT AGG TCA GAA AAG Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys 1345 1350 1355 1360 | 4080 |
| CTA CAT AAC ACT ACA GTA GAA CTT GCC ATT CTC ATT GAT ACC ATT AAT Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Thr Ile Asn 1365 1370 1375 | 4128 |
| AAT ACA TTA GTC AAT CTT GAA TGG CTC AAT AGA ATT GAA ACT TAT GTA Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val 1380 1385 1390 | 4176 |
| AAA TGG CCT TGG TAT GTG TGG CTA CTG ATA GGT CTA GTA GTA GTA TTT Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Val Phe 1395 1400 1405 | 4224 |
| TGC ATA CCA TTA CTG CTA TTT TGC TGT TTT AGC ACA GGT TGT TGT GGA Cys Ile Pro Leu Leu Phe Cys Cys Phe Ser Thr Gly Cys Cys Gly 1410 1415 1420 | 4272 |
| TGC ATA GGT TGT TTA GGA AGT TGT TGT CAC TCT ATA TGT AGT AGA AGA Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg 1425 1430 1435 1440 | 4320 |
| CAA TTT GAA TAT TAT GAA CCA ATT GAA AAA GTG CAT GTC CAC Gln Phe Glu Tyr Tyr Glu Pro Ile Glu Lys Val His Val His 1445 1450 | 4362 |
| TAA | 4365 |

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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| Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr 1 5 10 15 |
| Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln 20 25 30 |
| Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe 35 40 45 |
| Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val 50 55 60 |
| Trp Tyr Asn Cys Ser Arg Thr Ala Gln Thr Thr Ala Phe Gln Tyr Phe 65 70 75 80 |
| Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser 85 90 95 |
| Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu 100 105 110 |
| Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln 115 120 125 |

Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg
 130 135 140
 His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys
 145 150 155 160
 Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn
 165 170 175
 Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala
 180 185 190
 Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe
 195 200 205
 Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu
 210 215 220
 Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr
 225 230 235 240
 Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp
 245 250 255
 Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser
 260 265 270
 Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu
 275 280 285
 Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro
 290 295 300
 Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala
 305 310 315 320
 Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val
 325 330 335
 Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr
 340 345 350
 Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr
 355 360 365
 Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser
 370 375 380
 Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp
 385 390 395 400
 Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr
 405 410 415
 Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp
 420 425 430
 Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile
 435 440 445
 Gly Cys Ile Ser Phe Asn Leu Thr Thr Gly Ala Ser Gly Ala Phe Trp
 450 455 460
 Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn
 465 470 475 480

Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile
485 490 495

Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val
500 505 510

Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro
515 520 525

Ser Phe Phe Thr His Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met
530 535 540

Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile
545 550 555 560

Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser
565 570 575

Asn Gln Phe Ser Val Tyr Val Pro Ser Thr Cys Lys Ser Ser Leu Trp
580 585 590

Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala
595 600 605

Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn
610 615 620

Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala
625 630 635 640

Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val
645 650 655

Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly
660 665 670

Val Pro Ser Asp Asn Ser Gly Leu His Asp Leu Ser Val Leu His Leu
675 680 685

Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile
690 695 700

Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser
705 710 715 720

Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile
725 730 735

Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp
740 745 750

Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly
755 760 765

Leu Thr His Trp Thr Thr Pro Asn Phe Tyr Tyr Tyr Ser Ile Tyr
770 775 780

Asn Tyr Thr Ser Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp
785 790 795 800

Val Asp Cys Glu Pro Val Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys
805 810 815

Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val
820 825 830

Gln Pro Ile Ser Thr Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile
 835 840 845
 Ser Val Gln Val Glu Tyr Met Gln Val Tyr Thr Pro Val Ser Ile
 850 855 860
 Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu
 865 870 875 880
 Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala
 885 890 895
 Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val
 900 905 910
 Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr
 915 920 925
 Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Ser Ile Gly Gly Ser
 930 935 940
 Trp Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg
 945 950 955 960
 Lys Tyr Gly Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr
 965 970 975
 Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly
 980 985 990
 Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met
 995 1000 1005
 Val Leu Pro Gly Val Ala Asn Ala Asp Lys Met Thr Met Tyr Thr Ala
 1010 1015 1020
 Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Ala Val
 1025 1030 1035 1040
 Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala
 1045 1050 1055
 Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala
 1060 1065 1070
 Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn
 1075 1080 1085
 Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala Thr Val Ala Lys Ala
 1090 1095 1100
 Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser
 1105 1110 1115 1120
 His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser
 1125 1130 1135
 Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln
 1140 1145 1150
 Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val
 1155 1160 1165
 Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu
 1170 1175 1180

Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe
 1185 1190 1195 1200
 Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala
 1205 1210 1215
 Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr
 1220 1225 1230
 Glu Thr Val Thr Ala Trp Ser Gly Ile Cys Ala Ser Asp Gly Asp Arg
 1235 1240 1245
 Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn
 1250 1255 1260
 Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg
 1265 1270 1275 1280
 Val Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu
 1285 1290 1295
 Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr
 1300 1305 1310
 Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro
 1315 1320 1325
 Asn Trp Thr Val Pro Glu Phe Thr Leu Asp Ile Phe Asn Ala Thr Tyr
 1330 1335 1340
 Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys
 1345 1350 1355 1360
 Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Thr Ile Asn
 1365 1370 1375
 Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val
 1380 1385 1390
 Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Val Phe
 1395 1400 1405
 Cys Ile Pro Leu Leu Leu Phe Cys Cys Phe Ser Thr Gly Cys Cys Gly
 1410 1415 1420
 Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg
 1425 1430 1435 1440
 Gln Phe Glu Tyr Tyr Glu Pro Ile Glu Lys Val His Val His
 1445 1450

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..2244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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|---|-----|
| ATG ATT GTG CTC GTA ACT TGC CTC TTG TTG TTA TGT TCA TAC CAC ACA | 48 |
| Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr | |
| 1 5 10 15 | |
| GTG TTG AGT ACA ACA AAT AAT GAA TGC ATA CAA GTT AAC GTA ACA CAA | 96 |
| Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln | |
| 20 25 30 | |
| TTG GCT GGC AAT GAA AAC CTT ATC AGA GAT TTT CTG TTT AGT AAC TTT | 144 |
| Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe | |
| 35 40 45 | |
| AAA GAA GAA GGA AGT GTA GTT GGT GGT TAT TAC CCT ACA GAG GTG | 192 |
| Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val | |
| 50 55 60 | |
| TGG TAC AAC TGC TCT AGA ACA GCT CGA ACT ACT GCC TTT CAG TAT TTT | 240 |
| Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe | |
| 65 70 75 80 | |
| AAT AAT ATA CAT GCC TTT TAT TTT GTT ATG GAA GCC ATG GAA AAT AGC | 288 |
| Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser | |
| 85 90 95 | |
| ACT GGT AAT GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG | 336 |
| Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu | |
| 100 105 110 | |
| CCT GTT AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA | 384 |
| Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln | |
| 115 120 125 | |
| CAA AGG CCC CTT TTA GAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC | 432 |
| Gln Arg Pro Leu Leu Glu His Gly Leu Val Cys Ile Thr Lys Asn Arg | |
| 130 135 140 | |
| CAT ATT AAC TAT GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT | 480 |
| His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys | |
| 145 150 155 160 | |
| ACG GGT GCT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT | 528 |
| Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn | |
| 165 170 175 | |
| GGA ACA AAA ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT | 576 |
| Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala | |
| 180 185 190 | |
| TAT ATT AGT GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT | 624 |
| Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe | |
| 195 200 205 | |
| AAC AAT GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GAA | 672 |
| Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu | |
| 210 215 220 | |
| TAC AGT GCT GCA TAT GCT TAC CAA GGT GTT TCT AAC TTC ACT TAT TAC | 720 |
| Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr | |
| 225 230 235 240 | |
| AAG TTA AAT AAC ACC AAT GGT CTA AAA ACC TAT GAA TTA TGT GAA GAT | 768 |
| Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp | |
| 245 250 255 | |

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|---|------|
| TAT GAA CAT TGC ACT GGC TAT GCT ACC AAT GTA TTT GCT CCG ACA TCA Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser 260 265 270 | 816 |
| GGT GGT TAC ATA CCT GAT GGA TTT AGT TTT AAT AAT TGG TTC TTG CTT Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu 275 280 285 | 864 |
| ACA AAT AGT TCC ACT TTT GTT AGT GGC AGG TTT GTA ACA AAT CAA CCA Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro 290 295 300 | 912 |
| TTA TTG ATT AAT TGC TTG TGG CCA GTG CCC AGT TTT GGT GTA GCA GCA Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala 305 310 315 320 | 960 |
| CAA GAA TTT TGT TTT GAA GGT GCA CAG TTT AGC CAA TGT AAT GGT GTG Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val 325 330 335 | 1008 |
| TCT TTA AAT AAC ACA GTG GAT GTT ATT AGA TTC AAC CTT AAT TTC ACT Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr 340 345 350 | 1056 |
| GCA GAT GTA CAA TCT GGT ATG GGT GCC ACA GTA TTT TCA CTG AAT ACA Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr 355 360 365 | 1104 |
| ACA GGT GGT GTC ATT CTT GAA ATT TCA TGT TAT AGT GAC ACA GTG AGT Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser 370 375 380 | 1152 |
| GAG TCT AGT TCT TAC AGT TAT GGT GAA ATC CCG TTC GGC ATA ACT GAC Glu Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp 385 390 395 400 | 1200 |
| GGA CCA CGA TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAA TAT Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr 405 410 415 | 1248 |
| TTA GGA ACA TTA CCA CCC AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp 420 425 430 | 1296 |
| GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445 | 1344 |
| GGT TGT ATA TCT TTT AAT TTA ACC ACT GGT GTT AGT GGA GCT TTT TGG Gly Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp 450 455 460 | 1392 |
| ACA ATT GCT TAC ACA TCG TAT ACT GAA GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480 | 1440 |
| ACA GCT ATT AAA AAT GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495 | 1488 |
| AAA TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510 | 1536 |
| GCT TCA AGT GAA GTA GGT TTC GTT AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525 | 1584 |

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| AGC TTT TTC ACA TAC ACC GCT GTC AAT ATA ACC ATT GAT CTT GGT ATG Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met 530 535 540 | 1632 |
| AAG CTT AGT GGT TAT GGT CAA CCC ATA GCC TCG ACA CTA AGT AAC ATC Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560 | 1680 |
| ACA CTA CCA ATG CAG GAT AAC AAT ACT GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575 | 1728 |
| AAC CAA TTC TCA GTT TAT GTT CAT TCC ACT TGC AAA AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp 580 585 590 | 1776 |
| GAC AAT ATC TTT AAT CAA GAC TGC ACG GAT GTT TTA GAG GCT ACA GCT Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala 595 600 605 | 1824 |
| GTT ATA AAA ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn 610 615 620 | 1872 |
| TAC TTG ACT TTT AAC AAG TTC TGT TTG TCG TTG AGT CCT GTT GGT GCT Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640 | 1920 |
| AAT TGC AAG TTT GAT GTT GCT GCA CGT ACA AGA ACC AAT GAG CAG GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655 | 1968 |
| GTT AGA AGT CTA TAT GTA ATA TAT GAA GAA GGA GAC AAC ATA GTG GGT Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670 | 2016 |
| GTA CCG TCT GAT GAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685 | 2064 |
| GAC TCC TGT ACA GAT TAC AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700 | 2112 |
| ATT AGA CGA ACT AAC AGT ACG CTA CTT AGT GGC TTA TAT TAC ACA TCA Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser 705 710 715 720 | 2160 |
| CTA TCA GGT GAT TTG TTA GGC TTT AAA AAT GTT AGT GAT GGT GTC ATT Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile 725 730 735 | 2208 |
| TAT TCT GTG ACG CCA TGT GAT GTA AGC GCA CAA GCG GC Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala 740 745 | 2246 |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr
1 5 10 15

Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln
20 25 30

Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe
35 40 45

Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val
50 55 60

Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe
65 70 75 80

Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser
85 90 95

Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu
100 105 110

Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln
115 120 125

Gln Arg Pro Leu Leu Glu His Gly Leu Val Cys Ile Thr Lys Asn Arg
130 135 140

His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys
145 150 155 160

Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn
165 170 175

Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala
180 185 190

Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe
195 200 205

Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu
210 215 220

Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr
225 230 235 240

Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp
245 250 255

Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser
260 265 270

Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu
275 280 285

Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro
290 295 300

Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala
305 310 315 320

Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val
325 330 335

Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr
340 345 350

Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr
 355 360 365
 Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser
 370 375 380
 Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp
 385 390 395 400
 Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr
 405 410 415
 Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp
 420 425 430
 Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile
 435 440 445
 Gly Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp
 450 455 460
 Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn
 465 470 475 480
 Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile
 485 490 495
 Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val
 500 505 510
 Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro
 515 520 525
 Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met
 530 535 540
 Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile
 545 550 555 560
 Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser
 565 570 575
 Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp
 580 585 590
 Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala
 595 600 605
 Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn
 610 615 620
 Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala
 625 630 635 640
 Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val
 645 650 655
 Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly
 660 665 670
 Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu
 675 680 685
 Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile
 690 695 700

Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser
 705 710 715 720
 Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile
 725 730 735
 Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala
 740 745

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..4362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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|---|------|
| ATG ATT GTG CTC GTA ACT TGC CTC TTG TTG TTA TGT TCA TAC CAC ACA | 48 |
| Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr | |
| 1 5 10 15 | |
| GTG TTG AGT ACA ACA AAT AAT GAA TGC ATA CAA GTT AAC GTT ACA CAA | 96 |
| Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln | |
| 20 25 30 | |
| TTG GCT GGC AAT GAA AAC CTT ATC AGA GAT TTT CTG TTT AGT AAC TTT | 144 |
| Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe | |
| 35 40 45 | |
| AAA GAA GAA GGA AGT GTA GTT GGT GGT TAT TAC CCT ACA GAG GTG | 192 |
| Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val | |
| 50 55 60 | |
| TGG TAC AAC TGC TCT AGA ACA GCT CGA ACT ACT GCC TTT CAG TAT TTT | 240. |
| Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Ala Phe Gln Tyr Phe | |
| 65 70 75 80 | |
| AAT AAT ATA CAT GCC TTT TAT TTT GTT ATG GAA GCC ATG GAA AAT AGC | 288 |
| Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser | |
| 85 90 95 | |
| ACT GGT AAT GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG | 336 |
| Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu | |
| 100 105 110 | |
| CCT GTT AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA | 384 |
| Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln | |
| 115 120 125 | |
| CAA AGG CCC CTT TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC | 432 |
| Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg | |
| 130 135 140 | |
| CAT ATT AAC TAT GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT | 480 |
| His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys | |
| 145 150 155 160 | |

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|---|------|
| ACG GGT GCT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT | 528 |
| Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn | |
| 165 170 175 | |
| GGA ACA AAA ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT | 576 |
| Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala | |
| 180 185 190 | |
| TAT ATT AGT GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT | 624 |
| Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe | |
| 195 200 205 | |
| AAC AAT GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GAA | 672 |
| Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu | |
| 210 215 220 | |
| TAC AGT GCT GCA TAT GCT TAC CAA GGT GTT TCT AAC TTC ACT TAT TAC | 720 |
| Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr | |
| 225 230 235 240 | |
| AAG TTA AAT AAC ACC AAT GGT CTA AAA ACC TAT GAA TTA TGT GAA GAT | 768 |
| Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp | |
| 245 250 255 | |
| TAT GAA CAT TGC ACT GGC TAT GCT ACC AAT GTA TTT GCT CCG ACA TCA | 816 |
| Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser | |
| 260 265 270 | |
| GGT GGT TAC ATA CCT GAT GGA TTT AGT TTT AAT AAT TGG TTC TTG CTT | 864 |
| Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu | |
| 275 280 285 | |
| ACA AAT AGT TCC ACT TTT GTT AGT GGC AGG TTT GTA ACA AAT CAA CCA | 912 |
| Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro | |
| 290 295 300 | |
| TTA TTG ATT AAT TGC TTG TGG CCA GTG CCC AGT TTT GGT GTA GTA GCA | 960 |
| Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Val Ala | |
| 305 310 315 320 | |
| CAA GAA TTT TGT TTT GAA GGT GCA CAG TTT AGC CAA TGT AAT GGT GTG | 1008 |
| Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val | |
| 325 330 335 | |
| TCT TTA AAT AAC ACA GTG GAT GTT ATT AGA TTC AAC CTT AAT TTC ACT | 1056 |
| Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr | |
| 340 345 350 | |
| GCA GAT GTA CAA TCT GGT ATG GGT GCT ACA GTA TTT TCA CTG AAT ACA | 1104 |
| Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr | |
| 355 360 365 | |
| ACA GGT GGT GTC ATT CTT GAA ATT TCA TGT TAT AGT GAC ACA GTG AGT | 1152 |
| Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser | |
| 370 375 380 | |
| GAG TCT AGT TCT TAC AGT TAT GGT GAA ATC CCG TTC GGC ATA ACT GAC | 1200 |
| Glu Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp | |
| 385 390 395 400 | |
| GGA CCA CGA TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAA TAT | 1248 |
| Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr | |
| 405 410 415 | |
| TTA GGA ACA TTA CCA CCC AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG | 1296 |
| Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp | |
| 420 425 430 | |

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|---|------|
| GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445 | 1344 |
| GAT TGT ATA TCT TTT AAT TTA ACC ACT GGT GTT AGT GGA GCT TTT TGG Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp 450 455 460 | 1392 |
| ACA ATT GCT TAC ACA TCG TAT ACT GAA GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480 | 1440 |
| ACA GCT ATT AAA AAT GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495 | 1488 |
| AAA TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510 | 1536 |
| GCT TCA AGT GAA GTA GGT TTC GTT AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525 | 1584 |
| AGC TTT TTC ACA TAC ACC GCT GTC AAT ATA ACC ATT GAT CTT GGT ATG Ser Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met 530 535 540 | 1632 |
| AAG CTT AGT GGT TAT GGT CAA CCC ATA GCC TCG ACA CTA AGT AAC ATC Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560 | 1680 |
| ACA CTA CCA ATG CAG GAT AAC AAT ACT GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575 | 1728 |
| AAC CAA TTC TCA GTT TAT GTT CAT TCC ACT TGC AAA AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp 580 585 590 | 1776 |
| GAC AAT ATT TTT AAT CAA GAC TGC ACG GAT GTT TTA GAG GCT ACA GCT Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala 595 600 605 | 1824 |
| GTT ATA AAA ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn 610 615 620 | 1872 |
| TAC TTG ACT TTT AAC ACG TTC TGT TTG TCG TTG AGT CCT GTT GGT GCT Tyr Leu Thr Phe Asn Thr Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640 | 1920 |
| AAT TGC AAG TTT GAT GTT GCT GCA CGT ACA AGA ACC AAT GAG CAG GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655 | 1968 |
| GTT AGA AGT CTA TAT ATA ATA TAT GAA GAA GGA GAC AAC ATA GTG GGT Val Arg Ser Leu Tyr Ile Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670 | 2016 |
| GTA CCG TCT GAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685 | 2064 |
| GAC TCC TGT ACA GAT TAC AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700 | 2112 |

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| ATT AGA CGA ACT AAC AGT ACG CTA CTT AGT GGC TTA TAT TAC ACA TCA Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser 705 710 715 720 | 2160 |
| CTA TCA GGT GAT TTG TTA GGC TTT AAA AAT GTT AGT GAT GGT GTC ATT Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile 725 730 735 | 2208 |
| TAT TCT GTG ACG CCA TGT GAT GTA AGC GCA CAA GCG GCT GTT ATT GAT Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp 740 745 750 | 2256 |
| GGT GCC ATA GTT GGA GCT ATG ACT TCC ATT AAC AGT GAA CTG TTA GGT Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly 755 760 765 | 2304 |
| CTA ATA CAT TGG ACA ACG ACA CCT AAT TTT TAT TAC TAC TCT ATA TAT Leu Ile His Trp Thr Thr Pro Asn Phe Tyr Tyr Tyr Ser Ile Tyr 770 775 780 | 2352 |
| AAT TAC ACA AGT GAG AGG ACT CGT GGC ACT GCA ATT GAC AGT AAC GAT Asn Tyr Thr Ser Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp 785 790 795 800 | 2400 |
| GTT GAT TGT GAA CCT GTC ATA ACC TAT TCT AAT ATA GGT GTT TGT AAA Val Asp Cys Glu Pro Val Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys 805 810 815 | 2448 |
| AAT GGT GCT TTG GTT TTT ATT AAC GTC ACA CAT TCT GAC GGA GAC GTG Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val 820 825 830 | 2496 |
| CAA CCA ATT AGC ACT GGT AAT GTC ACG ATA CCT ACA AAT TTT ACC ATA Gln Pro Ile Ser Thr Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile 835 840 845 | 2544 |
| TCT GTG CAA GTT GAA TAC ATG CAG GTT TAC ACT ACA CCA GTA TCA ATA Ser Val Gln Val Glu Tyr Met Gln Val Tyr Thr Thr Pro Val Ser Ile 850 855 860 | 2592 |
| GAT TGT GCA AGA TAC GTT TGT AAT GGT AAC CCT AGA TGT AAC AAA TTG Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu 865 870 875 880 | 2640 |
| TTA ACA CAA TAT GTG TCT GCA TGT CAA ACT ATT GAA CAA GCA CTT GCA Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala 885 890 895 | 2688 |
| ATG GGT GCC AGA CTT GAA AAC ATG GAG GTT GAT TCC ATG TTG TTT GTC Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val 900 905 910 | 2736 |
| TCG GAA AAT GCC CTT AAA TTG GCA TCT GTT GAG GCG TTC AAT AGT ACA Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr 915 920 925 | 2784 |
| GAA AAT TTA GAT CCT ATT TAC AAA GAA TGG CCT AGC ATA GGT GGT TCT Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Ser Ile Gly Gly Ser 930 935 940 | 2832 |
| TGG CTA GGA GGT CTA AAA GAT ATA CTA CCG TCC CAT AAT AGC AAA CGT Trp Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg 945 950 955 960 | 2880 |
| AAG TAT GGT TCT GCT ATA GAA GAT TTG CTT TTT GAT AAA GTT GTA ACA Lys Tyr Gly Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr 965 970 975 | 2928 |

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| TCT GGT TTA GGT ACA GTT GAT GAA GAT TAT AAA CGT TGT ACT GGT GGT Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly 980 985 990 | 2976 |
| TAC GAC ATA GCA GAC TTG GTG TGT GCT CAA TAT TAC AAT GGC ATC ATG Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met 995 1000 1005 | 3024 |
| GTT CTA CCA GGT GTA GCT AAT GCT GAC AAG ATG ACT ATG TAC ACA GCA Val Leu Pro Gly Val Ala Asn Ala Asp Lys Met Thr Met Tyr Thr Ala 1010 1015 1020 | 3072 |
| TCA CTT GCA GGT GGT ATA ACA TTA GGT GCA CTT GGT GGT GGC GCC GTG Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Ala Val 1025 1030 1035 1040 | 3120 |
| GCT ATA CCT TTT GCA GTA GCA GTA CAG GCT AGA CTT AAT TAT GTT GCT Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala 1045 1050 1055 | 3168 |
| CTA CAA ACT GAT GTA TTG AAT AAA AAC CAA CAG ATC CTG GCT AAT GCT Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala 1060 1065 1070 | 3216 |
| TTC AAT CAA GCT ATT GGT AAC ATT ACA CAG GCT TTT GGT AAG GTT AAT Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn 1075 1080 1085 | 3264 |
| GAT GCT ATA CAT CAA ACA TCA CAA GGT CTT GCC ACT GTT GCT AAA GCG Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala Thr Val Ala Lys Ala 1090 1095 1100 | 3312 |
| TTG GCA AAA GTG CAA GAT GTT GTC AAC ACA CAA GGG CAA GCT TTA AGT Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser 1105 1110 1115 1120 | 3360 |
| CAC CTT ACA GTA CAA TTG CAA AAT AAT TTT CAA GCC ATT AGT AGT TCT His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser 1125 1130 1135 | 3408 |
| ATT AGT GAT ATT TAT AAC AGG CTT GAC GAA CTG AGT GCT GAT GCA CAA Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln 1140 1145 1150 | 3456 |
| GTT GAT AGG CTG ATT ACA GGT AGA CTT ACA GCA CTT AAT GCA TTT GTG Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val 1155 1160 1165 | 3504 |
| TCT CAG ACT CTA ACC AGA CAA GCA GAG GTT AGG GCT AGT AGA CAA CTT Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu 1170 1175 1180 | 3552 |
| GCC AAA GAC AAG GTT AAT GAA TGT GTT AGG TCT CAG TCT CAG AGA TTC Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe 1185 1190 1195 1200 | 3600 |
| GGA TTC TGT GGT AAT GGT ACA CAT TTG TTT TCA CTA GCA AAT GCA GCA Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala 1205 1210 1215 | 3648 |
| CCA AAT GGC ATG ATT TTC TTT CAT ACA GTA CTA TTA CCA ACA GCT TAT Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr 1220 1225 1230 | 3696 |
| GAA ACT GTA ACA GCT TGG TCA GGT ATT TGT GCT TCA GAT GGC GAT CGC Glu Thr Val Thr Ala Trp Ser Gly Ile Cys Ala Ser Asp Gly Asp Arg 1235 1240 1245 | 3744 |

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| ACT TTC GGA CTT GTC GTT AAA GAT GTG CAG TTG ACG TTG TTT CGT AAT | 3792 |
| Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn | |
| 1250 1255 1260 | |
| CTA GAT GAC AAG TTC TAT TTG ACC CCC AGA ACT ATG TAT CAG CCT AGA | 3840 |
| Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg | |
| 1265 1270 1275 1280 | |
| GTT GCA ACT AGT TCT GAT TTT GTT CAA ATT GAA GGG TGT GAT GTG TTG | 3888 |
| Val Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu | |
| 1285 1290 1295 | |
| TTT GTC AAC GCG ACT GTA ATT GAT TTG CCT AGT ATT ATA CCT GAC TAT | 3936 |
| Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr | |
| 1300 1305 1310 | |
| ATT GAC ATT AAT CAA ACT GTT CAA GAC ATA TTA GAA AAT TAC AGA CCA | 3984 |
| Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro | |
| 1315 1320 1325 | |
| AAC TGG ACT GTA CCT GAA TTT ACA CTT GAT ATT TTC AAC ACA ACC TAT | 4032 |
| Asn Trp Thr Val Pro Glu Phe Thr Leu Asp Ile Phe Asn Thr Thr Tyr | |
| 1330 1335 1340 | |
| TTA AAT CTG ACT GGT GAA ATT GAT GAC TTA GAG TTT AGG TCG GAA AAG | 4080 |
| Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys | |
| 1345 1350 1355 1360 | |
| CTA CAT AAC ACT ACA GTA GAA CTT GCC ATT CTC ATT GAT AAC ATT AAT | 4128 |
| Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Asn Ile Asn | |
| 1365 1370 1375 | |
| AAT ACA TTA GTC AAT CTT GAA TGG CTC AAT AGA ATT GAA ACT TAT GTA | 4176 |
| Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val | |
| 1380 1385 1390 | |
| AAA TGG CCT TGG TAT GTG TGG CTA CTG ATA GGT TTA GTA GTA GTA TTT | 4224 |
| Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Val Phe | |
| 1395 1400 1405 | |
| TGC ATA CCA TTA CTG CTA TTT TGC TGT TTT AGC ACA GGT TGT TGT GGA | 4272 |
| Cys Ile Pro Leu Leu Phe Cys Cys Phe Ser Thr Gly Cys Cys Gly | |
| 1410 1415 1420 | |
| TGC ATA GGT TGT TTA GGA AGT TGT TGT CAC TCT ATA TGT AGT AGA AGA | 4320 |
| Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg | |
| 1425 1430 1435 1440 | |
| CAA TTT GAA AAT TAT GAA CCA ATT GAA AAA GTG CAT GTC CAC | 4362 |
| Gln Phe Glu Asn Tyr Glu Pro Ile Glu Lys Val His Val His | |
| 1445 1450 | |
| TAA | 4365 |

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr
1 5 10 15

Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln
20 25 30

Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe
35 40 45

Lys Glu Glu Gly Ser Val Val Gly Gly Tyr Tyr Pro Thr Glu Val
50 55 60

Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe
65 70 75 80

Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser
85 90 95

Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu
100 105 110

Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln
115 120 125

Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg
130 135 140

His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys
145 150 155 160

Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn
165 170 175

Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala
180 185 190

Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe
195 200 205

Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu
210 215 220

Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr
225 230 235 240

Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp
245 250 255

Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser
260 265 270

Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu
275 280 285

Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro
290 295 300

Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Val Ala
305 310 315 320

Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val
325 330 335

Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr
340 345 350

Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr
355 360 365

Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser
370 375 380

Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp
385 390 395 400

Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr
405 410 415

Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp
420 425 430

Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile
435 440 445

Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp
450 455 460

Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn
465 470 475 480

Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile
485 490 495

Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val
500 505 510

Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro
515 520 525

Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met
530 535 540

Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile
545 550 555 560

Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser
565 570 575

Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp
580 585 590

Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala
595 600 605

Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn
610 615 620

Tyr Leu Thr Phe Asn Thr Phe Cys Leu Ser Leu Ser Pro Val Gly Ala
625 630 635 640

Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val
645 650 655

Val Arg Ser Leu Tyr Ile Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly
660 665 670

Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu
675 680 685

Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile
690 695 700

111

Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser
705 710 715 720
Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile
725 730 735
Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp
740 745 750
Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly
755 760 765
Leu Ile His Trp Thr Thr Pro Asn Phe Tyr Tyr Ser Ile Tyr
770 775 780
Asn Tyr Thr Ser Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp
785 790 795 800
Val Asp Cys Glu Pro Val Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys
805 810 815
Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val
820 825 830
Gln Pro Ile Ser Thr Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile
835 840 845
Ser Val Gln Val Glu Tyr Met Gln Val Tyr Thr Pro Val Ser Ile
850 855 860
Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu
865 870 875 880
Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala
885 890 895
Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val
900 905 910
Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr
915 920 925
Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Ser Ile Gly Gly Ser
930 935 940
Trp Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg
945 950 955 960
Lys Tyr Gly Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr
965 970 975
Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly
980 985 990
Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met
995 1000 1005
Val Leu Pro Gly Val Ala Asn Ala Asp Lys Met Thr Met Tyr Thr Ala
1010 1015 1020
Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Ala Val
1025 1030 1035 1040
Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala
1045 1050 1055

112

Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala
1060 1065 1070

Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn
1075 1080 1085

Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala Thr Val Ala Lys Ala
1090 1095 1100

Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser
1105 1110 1115 1120

His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser
1125 1130 1135

Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln
1140 1145 1150

Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val
1155 1160 1165

Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu
1170 1175 1180

Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe
1185 1190 1195 1200

Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala
1205 1210 1215

Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr
1220 1225 1230

Glu Thr Val Thr Ala Trp Ser Gly Ile Cys Ala Ser Asp Gly Asp Arg
1235 1240 1245

Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn
1250 1255 1260

Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg
1265 1270 1275 1280

Val Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu
1285 1290 1295

Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr
1300 1305 1310

Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro
1315 1320 1325

Asn Trp Thr Val Pro Glu Phe Thr Leu Asp Ile Phe Asn Thr Thr Tyr
1330 1335 1340

Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys
1345 1350 1355 1360

Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Asn Ile Asn
1365 1370 1375

Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val
1380 1385 1390

Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Val Phe
1395 1400 1405

113

Cys Ile Pro Leu Leu Leu Phe Cys Cys Phe Ser Thr Gly Cys Cys Gly
 1410 1415 1420

Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg
 1425 1430 1435 1440

Gln Phe Glu Asn Tyr Glu Pro Ile Glu Lys Val His Val His
 1445 1450

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | |
|---|-----|
| ATG ATT GTG CTC GTA ACT TGC CTC TTG TTG TTA TGT TCA TAC CAC ACA | 48 |
| Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr | |
| 1 5 10 15 | |
| | |
| GTT TTG AGT ACA ACA AAT AAT GAA TGC ATA CAA GTT AAC GTA ACA CAA | 96 |
| Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln | |
| 20 25 30 | |
| | |
| TTG GCT GGC AAT GAA AAC CTT ATC AGA GAT TTT CTG TTT AGT AAC TTT | 144 |
| Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe | |
| 35 40 45 | |
| | |
| AAA GAA GAA GGA AGT GTA GTT GGT GGT TAT TAC CCT ACA GAG GTG | 192 |
| Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val | |
| 50 55 60 | |
| | |
| TGG TAC AAC TGC TCT AGA ACA GCT CGA ACT ACT GCC TTT CAG TAT TTT | 240 |
| Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Ala Phe Gln Tyr Phe | |
| 65 70 75 80 | |
| | |
| AAT AAT ATA CAT GCC TTT TAT TTT GTT ATG GAA GCC ATG GAA AAT AGC | 288 |
| Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser | |
| 85 90 95 | |
| | |
| ACT GGT AAT GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG | 336 |
| Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu | |
| 100 105 110 | |
| | |
| CCT GTT AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA | 384 |
| Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln | |
| 115 120 125 | |
| | |
| CAA AGG CCC CTT TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC | 432 |
| Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg | |
| 130 135 140 | |
| | |
| CAT ATT AAC TAT GAA CAA TTC ACC AAC CAG TGG AAT TCC ACA TGT | 480 |
| His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys | |
| 145 150 155 160 | |

| | |
|---|------|
| ACG GGT GCT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT | 528 |
| Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn | |
| 165 170 175 | |
| GGA ACA AAA ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT | 576 |
| Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala | |
| 180 185 190 | |
| TAT ATT AGT GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT | 624 |
| Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe | |
| 195 200 205 | |
| AAC AAT GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GAA | 672 |
| Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu | |
| 210 215 220 | |
| TAC AGT GCT GCA TAT GCT TAC CAA GGT GTT TCT AAC TTC ACT TAT TAC | 720 |
| Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr | |
| 225 230 235 240 | |
| AAG TTA AAT AAC ACC AAT GGT CTA AAA ACC TAT GAA TTA TGT GAA GAT | 768 |
| Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp | |
| 245 250 255 | |
| TAT GAA CAT TGC ACT GGC TAT GCT ACC AAT GTA TTT GCT CCG ACA TCA | 816 |
| Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser | |
| 260 265 270 | |
| GGT GGT TAC ATA CCT GAT GGA TTT AGT TTT AAT AAT TGG TTC TTG CTT | 864 |
| Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu | |
| 275 280 285 | |
| ACA AAT AGT TCC ACT TTT GTT AGT GGC AGG TTT GTA ACA AAT CAA CCA | 912 |
| Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro | |
| 290 295 300 | |
| TTA TTG ATT AAT TGC TTG TGG CCA GTG CCC AGT TTT GGT GTA GCA GCA | 960 |
| Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala | |
| 305 310 315 320 | |
| CAA GAA TTT TGT TTT GAA GGT GCA CAG TTT AGC CAA TGT AAT GGT GTG | 1008 |
| Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val | |
| 325 330 335 | |
| TCT TTA AAT AAC ACA GTG GAT GTT ATT AGA TTC AAC CTT AAT TTC ACT | 1056 |
| Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr | |
| 340 345 350 | |
| GCA GAT GTA CAA TCT GGT ATG GGT GCT ACA GTA TTT TCA CTG AAT ACA | 1104 |
| Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr | |
| 355 360 365 | |
| ACA GGT GGT GTC ATT CTT GAA ATT TCA TGT TAT AGT GAC ACA GTG AGT | 1152 |
| Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser | |
| 370 375 380 | |
| GAG TCT AGT TCT TAC AGT TAT GGT GAA ATC CCG TTC GGC ATA ACT GAC | 1200 |
| Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp | |
| 385 390 395 400 | |
| GGA CCA CGA TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAA TAT | 1248 |
| Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr | |
| 405 410 415 | |
| TTA GGA ACA TTA CCA CCC AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG | 1296 |
| Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp | |
| 420 425 430 | |

| | |
|---|------|
| GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445 | 1344 |
| GAT TGT ATA TCT TTT AAT TTA ACC ACT GGT GTT AGT GGA GCT TTT TGG Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp 450 455 460 | 1392 |
| ACA ATT GCT TAC ACA TCG TAT ACT GAA GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480 | 1440 |
| ACA GCT ATT AAA AAT GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495 | 1488 |
| AAA TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510 | 1536 |
| GCT TCA AGT GAA GTA GGT TTC GTT AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525 | 1584 |
| AGC TTT TTC ACA TAC ACC GCT GTC AAT ATA ACC ATT GAT CTT GGT ATG Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met 530 535 540 | 1632 |
| AAG CTT AGT GGT TAT GGT CAA CCC ATA GCC TCG ACA CTA AGT AAC ATC Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560 | 1680 |
| ACA CTA CCA ATG CAG GAT AAC AAT ACT GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575 | 1728 |
| AAC CAA TTC TCA GTT TAT GTT CAT TCC ACT TGC AAA AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp 580 585 590 | 1776 |
| GAC AAT ATT TTT AAT CAA GAC TGC ACG GAT GTT TTA GAG GCT ACA GCT Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala 595 600 605 | 1824 |
| GTT ATA AAA ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn 610 615 620 | 1872 |
| TAC TTG ACT TTT AAC AAG TTC TGT TTG TCG TTG AGT CCT GTT GGT GCT Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640 | 1920 |
| AAT TGC AAG TTT GAT GTT GCT GCA CGT ACA AGA ACC AAT GAG CAG GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655 | 1968 |
| GTT AGA AGT CTA TAT GTA ATA TAT GAA GAA GGA GAC AAC ATA GTG GGT Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670 | 2016 |
| GTA CCG TCT GAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685 | 2064 |
| GAC TCC TGT ACA GAT TAC AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700 | 2112 |

| | |
|---|------|
| ATT AGA CGA ACT AAC AGT ACG CTA CTT AGT GGC TTA TAT TAC ACA TCA | 2160 |
| Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser | |
| 705 710 715 720 | |
| CTA TCA GGT GAT TTG TTA GGC TTT AAA AAT GTT AGT GAT GGT GTC ATT | 2208 |
| Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile | |
| 725 730 735 | |
| TAT TCT GTG ACG CCA TGT GAT GTA AGC GCA CAA GCG GC | 2246 |
| Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala | |
| 740 745 | |

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|---|--|
| Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr | |
| 1 5 10 15 | |
| Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln | |
| 20 25 30 | |
| Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe | |
| 35 40 45 | |
| Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val | |
| 50 55 60 | |
| Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe | |
| 65 70 75 80 | |
| Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser | |
| 85 90 95 | |
| Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu | |
| 100 105 110 | |
| Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln | |
| 115 120 125 | |
| Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg | |
| 130 135 140 | |
| His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys | |
| 145 150 155 160 | |
| Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn | |
| 165 170 175 | |
| Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala | |
| 180 185 190 | |
| Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe | |
| 195 200 205 | |
| Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu | |
| 210 215 220 | |

Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr
225 230 235 240
Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp
245 250 255
Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser
260 265 270
Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu
275 280 285
Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro
290 295 300
Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala
305 310 315 320
Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val
325 330 335
Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr
340 345 350
Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr
355 360 365
Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser
370 375 380
Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp
385 390 395 400
Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr
405 410 415
Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp
420 425 430
Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile
435 440 445
Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp
450 455 460
Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn
465 470 475 480
Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile
485 490 495
Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val
500 505 510
Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro
515 520 525
Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met
530 535 540
Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile
545 550 555 560
Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser
565 570 575

Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp
 580 585 590
 Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala
 595 600 605
 Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn
 610 615 620
 Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala
 625 630 635 640
 Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val
 645 650 655
 Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly
 660 665 670
 Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu
 675 680 685
 Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile
 690 695 700
 Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser
 705 710 715 720
 Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile
 725 730 735
 Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala
 740 745

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | |
|---|-----|
| GT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG CCT GTT AGT GTT | 47 |
| Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val Ser Val | |
| 1 5 10 15 | |
| ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA CAA AGG CCC CTT | 95 |
| Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg Pro Leu | |
| 20 25 30 | |
| TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC CAT ATT AAC TAT | 143 |
| Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile Asn Tyr | |
| 35 40 45 | |
| GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT ACG GGT GCT GAC | 191 |
| Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly Ala Asp | |
| 50 55 60 | |

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|---|-----|
| AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT GGA ACA AAA ATC | 239 |
| Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr Lys Ile | |
| 65 70 75 | |
| TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT TAT ATT AGT GGT | 287 |
| Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile Ser Gly | |
| 80 85 90 95 | |
| CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT AAC AAT GTC ACA | 335 |
| Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn Val Thr | |
| 100 105 110 | |
| CTT TTG TAT TCA CGC TCA AGC ATT GCT ACC TGG GA | 370 |
| Leu Leu Tyr Ser Arg Ser Ser Ile Ala Thr Trp | |
| 115 120 | |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

| | |
|---|--|
| Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val Ser Val Ile | |
| 1 5 10 15 | |
| Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg Pro Leu Leu | |
| 20 25 30 | |
| Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile Asn Tyr Glu | |
| 35 40 45 | |
| Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly Ala Asp Arg | |
| 50 55 60 | |
| Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr Lys Ile Tyr | |
| 65 70 75 80 | |
| Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile Ser Gly Arg | |
| 85 90 95 | |
| Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn Val Thr Leu | |
| 100 105 110 | |
| Leu Tyr Ser Arg Ser Ser Ile Ala Thr Trp | |
| 115 120 | |

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..4362

120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | |
|---|-----|
| ATG ATT GTG CTC GTA ACT TGC CTC TTG TTG TTA TGC TCA TAC CAC ACT | 48 |
| Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr | |
| 1 5 10 15 | |
| GTT TCG AGT ACG TCA AAC AAT GAT TGT AGA CAA GTT AAC GTA ACA CAA | 96 |
| Val Ser Ser Thr Ser Asn Asn Asp Cys Arg Gln Val Asn Val Thr Gln | |
| 20 25 30 | |
| TTA GCT GGC AAT GAA AAC CTT ATT AGA GAC TTT TTG TTT CAA AGT TTT | 144 |
| Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Gln Ser Phe | |
| 35 40 45 | |
| AAA GAA GAA GGA ATT GTA GTT GGT GGT TAT TAC CCT ACA GAG GTG | 192 |
| Lys Glu Glu Gly Ile Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val | |
| 50 55 60 | |
| TGG TAC AAC TGC TCT AGA ACA GCA ACT ACC ACT GCC TAT GAG TAT TTT | 240 |
| Trp Tyr Asn Cys Ser Arg Thr Ala Thr Thr Ala Tyr Glu Tyr Phe | |
| 65 70 75 80 | |
| AAT AAT ATA CAT GCC TTT TAT TTT GAT ATG GAA GCT ATG GAA AAT AGC | 288 |
| Asn Asn Ile His Ala Phe Tyr Phe Asp Met Glu Ala Met Glu Asn Ser | |
| 85 90 95 | |
| ACT GGT AAT GCA CGT GGT AAA CCT CTA TTA TTT CAT GTT CAT GGT GAA | 336 |
| Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu | |
| 100 105 110 | |
| CCT GTT AGT ATC ATC ATA TAT ATA TCA GCT TAT GGG GAT GAT GTG CAA | 384 |
| Pro Val Ser Ile Ile Ile Tyr Ile Ser Ala Tyr Gly Asp Asp Val Gln | |
| 115 120 125 | |
| CAA AGG CCA CTT TTA GAA CAT GGG TTA TTG TGC ATT ACT AAA AAT CGC | 432 |
| Gln Arg Pro Leu Leu Glu His Gly Leu Leu Cys Ile Thr Lys Asn Arg | |
| 130 135 140 | |
| AAT ATT GAC TAT AAC ACC TTC ACC AGC AAC CAG TGG GAT TCC ATA TGT | 480 |
| Asn Ile Asp Tyr Asn Thr Phe Thr Ser Asn Gln Trp Asp Ser Ile Cys | |
| 145 150 155 160 | |
| ACG GGT AAT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC AGG GAT AAT | 528 |
| Thr Gly Asn Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Arg Asp Asn | |
| 165 170 175 | |
| GGA ACA AAA ATC TAT GGG CTT GAG TGG AAT GAT GAA TTT GTT ACA GCG | 576 |
| Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Glu Phe Val Thr Ala | |
| 180 185 190 | |
| TAT ATT AGT GGT CGT TCT TAT AAT TGG AAC ATC AAT AAT AAC TGG TTT | 624 |
| Tyr Ile Ser Gly Arg Ser Tyr Asn Trp Asn Ile Asn Asn Asn Trp Phe | |
| 195 200 205 | |
| AAC AAT GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GAA | 672 |
| Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu | |
| 210 215 220 | |
| TAC AGT GCT GCA TAT GTT TAC CAA GGT GTT TCT AAC TTC ACT TAT TAC | 720 |
| Tyr Ser Ala Ala Tyr Val Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr | |
| 225 230 235 240 | |
| AAG TTA AAT AAC ACC AAT GGT TTA AAA ACC TAT GAA TTT TGT GAG GAT | 768 |
| Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Phe Cys Glu Asp | |
| 245 250 255 | |

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|---|------|
| TAT GAA TAT TGC ACT GGC TAC GCC ACT AAT GTC TTT GCT CCA ACT GTG Tyr Glu Tyr Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Val 260 265 270 | 816 |
| GGA GGT TAC ATA CCT GAT GGA TTT AGT TTT AAC AAT TGG TTT TTG CTT Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu 275 280 285 | 864 |
| ACA AAT AGC TCC ACT TTT GTT AGT GGC AGA TTT GTA ACA AAC CAA CCA Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro 290 295 300 | 912 |
| CTA TTA GTT AAC TGC TTA TGG CCA GTG CCC AGT TTT GGT GTA GCA GCA Leu Leu Val Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala 305 310 315 320 | 960 |
| CAA GAA TTT TGT TTT GAA GGT GCG CAG TTT AGT CAG TGT AGT GGT GTA Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Ser Gly Val 325 330 335 | 1008 |
| TCT TTA AAT AAC ACA GTA GAT GTT ATT AGA TTC AAT CTT AAT TTC ACC Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr 340 345 350 | 1056 |
| GCA GAT GTA CAA TCT GGT ATG GGT GCT ACA GTG TTT TCG TTG AAT ACA Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr 355 360 365 | 1104 |
| ACG GGT GGT GTC ATT CTT GAA GTT TCA TGT TAT AAT GAC ACA GTG AGT Thr Gly Gly Val Ile Leu Glu Val Ser Cys Tyr Asn Asp Thr Val Ser 370 375 380 | 1152 |
| GAG TCT AGT TTT TAC AGT TAT GGT GAA ATT CCG TTC GGC ATA ACT GAT Glu Ser Ser Phe Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp 385 390 395 400 | 1200 |
| GGA CCA CGG TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAG TAT Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr 405 410 415 | 1248 |
| TTA GGA ACA TTA CCA CCT AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp 420 425 430 | 1296 |
| GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445 | 1344 |
| GAT TGT ATA TCT TTT AAC TTA ACC ACT GGT GAT AGT GGA GCT TTT TGG Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Asp Ser Gly Ala Phe Trp 450 455 460 | 1392 |
| ACA ATT GCT TAC ACA TCG TAC ACT GAG GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480 | 1440 |
| ACA GCT ATT AAA AAG GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Lys Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495 | 1488 |
| AAG TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510 | 1536 |
| GCT TCA AGT GAG GTT GGT CTT GTG AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Leu Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525 | 1584 |

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|---|------|
| ATC TTT TTC GCA CAT ACC GCT ATC AAT ATA ACC ATT GAT CTT GGT ATG Ile Phe Phe Ala His Thr Ala Ile Asn Ile Thr Ile Asp Leu Gly Met 530 535 540 | 1632 |
| AAG CGT AGC GGT TAT GGT CAA CCC ATA GCA TCA ACA TTA AGT AAC ATT Lys Arg Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560 | 1680 |
| ACA CTA CCA ATG CAG GAT AAT AAC ACA GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575 | 1728 |
| AAC CAG TTT TCA GTT TAT GTT CAT TCT ATT TGT AAG AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val His Ser Ile Cys Lys Ser Ser Leu Trp 580 585 590 | 1776 |
| GAC AAT ATT TTT AAT CAA GAA TGC ACG GAT GTT TTA GAT GCC ACA GCT Asp Asn Ile Phe Asn Gln Glu Cys Thr Asp Val Leu Asp Ala Thr Ala 595 600 605 | 1824 |
| GTT ATA AAG ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn 610 615 620 | 1872 |
| TAC TTA ACT TTT AAC AAG TTC TGT TTG TCG TTG AGT CCT GTT GGC GCT Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640 | 1920 |
| AAC TGC AAG TTT GAT GTT GCC GCA CGT ACA AGA ACC AAT GAG CAA GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655 | 1968 |
| GTT AGA AGT CTA TAT GTA ATA TAT GAA GAA GGA GAC AAC ATA GTT GGT Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670 | 2016 |
| GTA CCG TCT GAT AAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asn Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685 | 2064 |
| GAC TCC TGT ACA GAG TAT AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Glu Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700 | 2112 |
| ATT AGA CAA ACT AAC AGT ACG CTA CTT AGC GGC TTA TAT TAC ACA TCA Ile Arg Gln Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser 705 710 715 720 | 2160 |
| CTA TCA GGT GAT TTG TTA GGC TTT AAA AAT GTT AGT GAT GGT GTC ATC Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile 725 730 735 | 2208 |
| TAT TCT GTG ACG CCA TGT GAT GTA AGC GCA CAA GCG GCT GTT ATT GAT Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp 740 745 750 | 2256 |
| GGT GCC ATA GTT GGA GCT ATG ACT TCC ATT AAC AGT GAA CTG TTA GGT Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly 755 760 765 | 2304 |
| CTA AAA CAC TGG ACA ACA ACA CCT AAT TTT TAT TAC TAC TCT ATA TAT Leu Lys His Trp Thr Thr Pro Asn Phe Tyr Tyr Tyr Ser Ile Tyr 770 775 780 | 2352 |
| AAT TAT ACA AAT GAG AGG ACT CGT GGC ACT GCA ATT GAC AGT AAC GAT Asn Tyr Thr Asn Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp 785 790 795 800 | 2400 |

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| GTT GAT TGT GAA CCT ATC ATA ACC TAT TCT AAC ATA GGT GTT TGT AAA Val Asp Cys Glu Pro Ile Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys 805 810 815 | 2448 |
| AAT GGT GCT TTG GTT TTT ATT AAC GTC ACA CAT TCT GAT GGA GAC GTG Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val 820 825 830 | 2496 |
| CAA CCA ATT AGC ACT GGT ACT GTC ACG ATA CCT ACA AAC TTT ACC ATA Gln Pro Ile Ser Thr Gly Thr Val Thr Ile Pro Thr Asn Phe Thr Ile 835 840 845 | 2544 |
| TCT GTG CAA GTC GAA TAC ATT CAG GTT TAC ACC ACA CCA GTA TCA ATA Ser Val Gln Val Glu Tyr Ile Gln Val Tyr Thr Thr Pro Val Ser Ile 850 855 860 | 2592 |
| GAT TGT GCA AGA TAC GTT TGC AAT GGT AAC CCT AGA TGT AAC AAA TTG Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu 865 870 875 880 | 2640 |
| TTA ACA CAA TAT GTT TCT GCA TGT CAA ACT ATT GAG CAA GCA CTT GCA Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala 885 890 895 | 2688 |
| ATG GGT GCC AGA CTT GAA AAC ATG GAG GTT GAT TCC ATG TTG TTC GTT Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val 900 905 910 | 2736 |
| TCT GAA AAT GCC CTT AAA TTG GCA TCT GTT GAG GCG TTC AAT AGT ACA Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr 915 920 925 | 2784 |
| GAA AAT TTA GAC CCT ATT TAC AAA GAA TGG CCT AAC ATA GGT GGT TCT Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Asn Ile Gly Gly Ser 930 935 940 | 2832 |
| TGG TTA GGA GGT TTA AAA GAC ATA CTG CCG TCC CAT AAT AGC AAA CGT Trp Leu Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg 945 950 955 960 | 2880 |
| AAG TAT CGT TCT GCT ATA GAA GAC TTG CTT TTT GAT AAG GTT GTA ACT Lys Tyr Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr 965 970 975 | 2928 |
| TCT GGT TTA GGT ACA GTT GAT GAA GAT TAT AAA CGT TGT ACA GGT GGT Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly 980 985 990 | 2976 |
| TAT GAC ATA GCC GAC TTA GTG TGT GCT CAA TAT TAC AAT GGC ATC ATG Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met 995 1000 1005 | 3024 |
| GTG TTA CCT GGT GTA GCT AAT GAT GAC AAG ATG ACT ATG TAC ACA GCA Val Leu Pro Gly Val Ala Asn Asp Asp Lys Met Thr Met Tyr Thr Ala 1010 1015 1020 | 3072 |
| TCT CTT GCA GGT GGT ATA ACA CTA GGT GCA CTT GGT GGT GGC GCC GTT Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Ala Val 1025 1030 1035 1040 | 3120 |
| GCT ATA CCT TTT GCA GTA GCA GTT CAA GCT AGA CTT AAT TAT GTT GCT Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala 1045 1050 1055 | 3168 |
| CTA CAA ACT GAT GTA TTG AAT AAA AAC CAG CAG ATC CTG GCT AAT GCT Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala 1060 1065 1070 | 3216 |

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| TTC AAT CAA GCT ATT GGT AAC ATT ACA CAG GCA TTT GGC AAG GTT AAT Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn 1075 1080 1085 | 3264 |
| GAT GCT ATA CAT CAA ACA TCA AAA GGT CTT GCA ACT GTT GCT AAA GCA Asp Ala Ile His Gln Thr Ser Lys Gly Leu Ala Thr Val Ala Lys Ala 1090 1095 1100 | 3312 |
| TTG GCA AAA GTG CAA GAT GTT GTC AAC ACA CAA GGG CAA GCT TTA AGC Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser 1105 1110 1115 1120 | 3360 |
| CAC CTA ACA GTA CAA TTG CAA AAT AAT TTT CAA GCC ATT AGT AGC TCT His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser 1125 1130 1135 | 3408 |
| ATT AGT GAT ATT TAT AAC AGG CTT GAC GAA CTG AGT GCT GAT GCA CAA Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln 1140 1145 1150 | 3456 |
| GTT GAT AGG CTG ATT ACA GGA AGA CTT ACA GCA CTT AAT GCA TTT GTG Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val 1155 1160 1165 | 3504 |
| TCT CAG ACT CTA ACC AGA CAA GCG GAG GTT AGG GCT AGT AGA CAA CTT Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu 1170 1175 1180 | 3552 |
| GCC AAG GAC AAG GTT AAT GAA TGT GTT AGA TCC CAA TCT CAG AGA TTT Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe 1185 1190 1195 1200 | 3600 |
| GGA TTC TGT GGT AAT GGT ACA CAC TTG TTT TCA CTT GCA AAT GCA GCA Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala 1205 1210 1215 | 3648 |
| CCA AAT GGC ATG ATT TTC TTT CAT ACA GTG CTA TTA CCA ACG GCT TAT Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr 1220 1225 1230 | 3696 |
| GAA ACT GTA ACA GCT TGG CCA GGT ATT TGT GCT TCA GAT GGC GAT CGC Glu Thr Val Thr Ala Trp Pro Gly Ile Cys Ala Ser Asp Gly Asp Arg 1235 1240 1245 | 3744 |
| ACT TTT GGA CTT GTC GTT AAA GAT GTA CAG TTG ACG TTG TTT CGT AAC Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn 1250 1255 1260 | 3792 |
| CTA GAT GAC AAG TTC TAT TTG ACT CCC AGA ACT ATG TAT CAG CCT AGA Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg 1265 1270 1275 1280 | 3840 |
| GCT GCA ACT AGT TCT GAT TTT GTT CAA ATT GAG GGG TGC GAT GTG TTG Ala Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu 1285 1290 1295 | 3888 |
| TTT GTC AAT GCA ACT GTA ATT GAC TTG CCT AGT ATT ATA CCT GAC TAT Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr 1300 1305 1310 | 3936 |
| ATT GAC ATC AAT CAG ACT GTT CAA GAT ATA TTA GAA AAT TAC AGA CCA Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro 1315 1320 1325 | 3984 |
| AAC TGG ACT GTA CCT GAA TTG ACA CTT GAT ATT TTT AAC GCA ACC TAT Asn Trp Thr Val Pro Glu Leu Thr Leu Asp Ile Phe Asn Ala Thr Tyr 1330 1335 1340 | 4032 |

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|---|------|
| TTA AAT CTG ACT GGT GAA ATT GAT GAC TTA GAA TTT AGG TCA GAA AAG Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys 1345 1350 1355 1360 | 4080 |
| CTA CAC AAT ACC ACT GTA GAA CTT GCC ATT CTC ATT GAC AAC ATT AAC Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Asn Ile Asn 1365 1370 1375 | 4128 |
| AAC ACA TTA GTC AAT CTT GAA TGG CTC AAT AGA ATT GAA ACT TAT GTA Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val 1380 1385 1390 | 4176 |
| AAA TGG CCT TGG TAT GTG TGG CTA CTA ATA GGC TTA GTA GTA ATA TTT Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Ile Phe 1395 1400 1405 | 4224 |
| TGC ATA CCA TTA TTG CTA TTT TGC TGT AGT ACA GGT TGT TGT GGA Cys Ile Pro Leu Leu Phe Cys Cys Cys Ser Thr Gly Cys Cys Gly 1410 1415 1420 | 4272 |
| TGC ATA GGT TGC TTA GGA AGT TGT TGT CAC TCT ATG TGT AGT AGA AGA Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Met Cys Ser Arg Arg 1425 1430 1435 1440 | 4320 |
| CAA TTT GAA AAT TAT GAA CCA ATT GAA AAA GTG CAT GTC CAC Gln Phe Glu Asn Tyr Glu Pro Ile Glu Lys Val His Val His 1445 1450 | 4362 |
| TAA | 4365 |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

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|--|
| Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr 1 5 10 15 |
| Val Ser Ser Thr Ser Asn Asn Asp Cys Arg Gln Val Asn Val Thr Gln 20 25 30 |
| Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Gln Ser Phe 35 40 45 |
| Lys Glu Glu Gly Ile Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val 50 55 60 |
| Trp Tyr Asn Cys Ser Arg Thr Ala Thr Thr Ala Tyr Glu Tyr Phe 65 70 75 80 |
| Asn Asn Ile His Ala Phe Tyr Phe Asp Met Glu Ala Met Glu Asn Ser 85 90 95 |
| Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu 100 105 110 |
| Pro Val Ser Ile Ile Ile Tyr Ile Ser Ala Tyr Gly Asp Asp Val Gln 115 120 125 |

Gln Arg Pro Leu Leu Glu His Gly Leu Leu Cys Ile Thr Lys Asn Arg
 130 135 140
 Asn Ile Asp Tyr Asn Thr Phe Thr Ser Asn Gln Trp Asp Ser Ile Cys
 145 150 155 160
 Thr Gly Asn Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Arg Asp Asn
 165 170 175
 Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Glu Phe Val Thr Ala
 180 185 190
 Tyr Ile Ser Gly Arg Ser Tyr Asn Trp Asn Ile Asn Asn Asn Trp Phe
 195 200 205
 Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu
 210 215 220
 Tyr Ser Ala Ala Tyr Val Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr
 225 230 235 240
 Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Phe Cys Glu Asp
 245 250 255
 Tyr Glu Tyr Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Val
 260 265 270
 Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu
 275 280 285
 Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro
 290 295 300
 Leu Leu Val Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala
 305 310 315 320
 Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Ser Gly Val
 325 330 335
 Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr
 340 345 350
 Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr
 355 360 365
 Thr Gly Gly Val Ile Leu Glu Val Ser Cys Tyr Asn Asp Thr Val Ser
 370 375 380
 Glu Ser Ser Phe Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp
 385 390 395 400
 Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr
 405 410 415
 Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp
 420 425 430
 Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile
 435 440 445
 Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Asp Ser Gly Ala Phe Trp
 450 455 460
 Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn
 465 470 475 480

Thr Ala Ile Lys Lys Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile
485 490 495

Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val
500 505 510

Ala Ser Ser Glu Val Gly Leu Val Asn Lys Ser Val Val Leu Leu Pro
515 520 525

Ile Phe Phe Ala His Thr Ala Ile Asn Ile Thr Ile Asp Leu Gly Met
530 535 540

Lys Arg Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile
545 550 555 560

Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser
565 570 575

Asn Gln Phe Ser Val Tyr Val His Ser Ile Cys Lys Ser Ser Leu Trp
580 585 590

Asp Asn Ile Phe Asn Gln Glu Cys Thr Asp Val Leu Asp Ala Thr Ala
595 600 605

Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn
610 615 620

Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala
625 630 635 640

Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val
645 650 655

Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly
660 665 670

Val Pro Ser Asp Asn Ser Gly Leu His Asp Leu Ser Val Leu His Leu
675 680 685

Asp Ser Cys Thr Glu Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile
690 695 700

Ile Arg Gln Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser
705 710 715 720

Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile
725 730 735

Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp
740 745 750

Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly
755 760 765

Leu Lys His Trp Thr Thr Pro Asn Phe Tyr Tyr Tyr Ser Ile Tyr
770 775 780

Asn Tyr Thr Asn Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp
785 790 795 800

Val Asp Cys Glu Pro Ile Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys
805 810 815

Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val
820 825 830

Gln Pro Ile Ser Thr Gly Thr Val Thr Ile Pro Thr Asn Phe Thr Ile
 835 840 845
 Ser Val Gln Val Glu Tyr Ile Gln Val Tyr Thr Thr Pro Val Ser Ile
 850 855 860
 Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu
 865 870 875 880
 Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala
 885 890 895
 Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val
 900 905 910
 Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr
 915 920 925
 Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Asn Ile Gly Gly Ser
 930 935 940
 Trp Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg
 945 950 955 960
 Lys Tyr Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr
 965 970 975
 Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly
 980 985 990
 Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met
 995 1000 1005
 Val Leu Pro Gly Val Ala Asn Asp Asp Lys Met Thr Met Tyr Thr Ala
 1010 1015 1020
 Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Ala Val
 1025 1030 1035 1040
 Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala
 1045 1050 1055
 Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala
 1060 1065 1070
 Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn
 1075 1080 1085
 Asp Ala Ile His Gln Thr Ser Lys Gly Leu Ala Thr Val Ala Lys Ala
 1090 1095 1100
 Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser
 1105 1110 1115 1120
 His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser
 1125 1130 1135
 Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln
 1140 1145 1150
 Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val
 1155 1160 1165
 Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu
 1170 1175 1180
 Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe

129

| 1185 | 1190 | 1195 | 1200 |
|---|------|------|------|
| Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala | | | |
| 1205 | 1210 | 1215 | |
| Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr | | | |
| 1220 | 1225 | 1230 | |
| Glu Thr Val Thr Ala Trp Pro Gly Ile Cys Ala Ser Asp Gly Asp Arg | | | |
| 1235 | 1240 | 1245 | |
| Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn | | | |
| 1250 | 1255 | 1260 | |
| Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg | | | |
| 1265 | 1270 | 1275 | 1280 |
| Ala Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu | | | |
| 1285 | 1290 | 1295 | |
| Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr | | | |
| 1300 | 1305 | 1310 | |
| Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro | | | |
| 1315 | 1320 | 1325 | |
| Asn Trp Thr Val Pro Glu Leu Thr Leu Asp Ile Phe Asn Ala Thr Tyr | | | |
| 1330 | 1335 | 1340 | |
| Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys | | | |
| 1345 | 1350 | 1355 | 1360 |
| Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Asn Ile Asn | | | |
| 1365 | 1370 | 1375 | |
| Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val | | | |
| 1380 | 1385 | 1390 | |
| Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Ile Phe | | | |
| 1395 | 1400 | 1405 | |
| Cys Ile Pro Leu Leu Leu Phe Cys Cys Cys Ser Thr Gly Cys Cys Gly | | | |
| 1410 | 1415 | 1420 | |
| Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Met Cys Ser Arg Arg | | | |
| 1425 | 1430 | 1435 | 1440 |
| Gln Phe Glu Asn Tyr Glu Pro Ile Glu Lys Val His Val His | | | |
| 1445 | 1450 | | |

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..2244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

| | |
|--|------|
| ATGATTGTGC TCGTAACCTG CCTCTTGTG TTATGTCAT ACCACACAGT TTTGAGTACA | 60 |
| ACAAATAATG AATGCATACA AGTTAACGTA ACACAATTGG CTGGCAATGA AAACCTTATC | 120 |
| AGAGATTTTC TGTTTAGTAA CTTTAAAGAA GAAGGAAGTG TAGTTGTTGG TGGTTATTAC | 180 |
| CCTACAGAGG TGTGGTACAA CTGCTCTAGA ACAGCTCGAA CTACTGCCTT TCAGTATTT | 240 |
| AATAATATAC ATGCCTTTA TTTTGTATG GAAGCCATGG AAAATAGCAC TGGTAATGCA | 300 |
| CGTGGTAAAC CATTATTATT TCATGTGCAT GGTGAGCCTG TTAGTGTAT TATATATATA | 360 |
| TCGGCTTATA GGGATGATGT GCAACAAAGG CCCCTTTAA AACATGGGTT AGTGTGCATA | 420 |
| ACTAAAAATC GCCATATTAA CTATGAACAA TTCACCTCCA ACCAGTGGAA TTCCACATGT | 480 |
| ACGGGTGCTG ACAGAAAAAT TCCTTCTCT GTCATACCCA CGGACAATGG AACAAAAATC | 540 |
| TATGGTCTTG AGTGGATGA TGACTTTGTT ACAGCTTATA TTAGTGGTCG TTCTTATCAC | 600 |
| TTGAACATCA ATACTAATTG GTTTAACAAAT GTCACACTTT TGTATTCAAG CTCAAGCACT | 660 |
| GCTACCTGGG AATACAGTGC TGCATATGCT TACCAAGGTG TTTCTAACTT CACTTATTAC | 720 |
| AAGTTAAATA ACACCAATGG TCTAAAAACC TATGAATTAT GTGAAGATTA TGAACATTGC | 780 |
| ACTGGCTATG CTACCAATGT ATTTGCTCCG ACATCAGGTG GTTACATACC TGATGGATT | 840 |
| AGTTTTAAYA ATTGGTTCTT GCTTACAAAT AGTTCCACTT TTGTTAGTGG CAGGTTGTA | 900 |
| ACAAATCAAC CATTATTGAT TAATTGCTTG TGGCCAGTGC CCAGTTTGG TGTAGCAGCA | 960 |
| CAAGAATTAA GTTTGAAGG TGCACAGTT AGCCAATGTA ATGGTGTGTC TTTAAATAAC | 1020 |
| ACAGTGGATG TTATTAGATT CAACCTTAAT TTCACTGCAG ATGTACAATC TGGTATGGGT | 1080 |
| GCTACAGTAT TTTCACTGAA TACAACAGGT GGTGTCATTC TTGAAATTTC ATGTTATAGT | 1140 |
| GACACAGTGA GTGAGTCTAG TTCTTACAGT TATGGTAAA TCCCCTTCGG CATAACTGAC | 1200 |
| GGACCACGAT ACTGTTATGT ACTTTACAAT GGCACAGCTC TTAAATATTT AGGAACATTA | 1260 |
| CCACCCAGTG TAAAGGAAAT TGCTATTAGT AAGTGGGCC ATTTTATAT TAATGGTTAC | 1320 |
| AATTCTTTA GCACATTCC TATTGRTTGT ATATCTTTA ATTTAACAC TGGTGTAGT | 1380 |
| GGAGCTTTT GGACAATTGC TTACACATCG TATACTGAAG CATTAGTACA AGTTGAAAAC | 1440 |
| ACAGCTATTA AAAATGTGAC GTATTGTAAC AGTCACATTA ATAACATTAA ATGTTCTCAA | 1500 |
| CTTACTGCTA ATTTGAATAA TGGATTTAT CCTGTTGCTT CAAGTGAAGT AGGTTCGTT | 1560 |
| AATAAGAGTG TTGTGTATT ACCTAGCTT TTCACATACA CCGCTGTCAA TATAACCATT | 1620 |
| GATCTTGGTA TGAAGCTTAG TGGTTATGGT CAACCCATAG CCTCGACACT AAGTAACATC | 1680 |
| ACACTACCAA TGCAGGATAA CAATACTGAT GTGTACTGTA TTCGTTCTAA CCAATTCTCA | 1740 |
| GTTTATGTC ATTCCACTTG CAAAAGTTCT TTATGGGACA ATATTTTAA TCAAGACTGC | 1800 |
| ACGGATGTTT TAGAGGCTAC AGCTGTTATA AAAACTGGTA CTTGTCCTT CTCATTGAT | 1860 |
| AAATTGAACA ATTACTTGAC TTTAACAAAG TTCTGTTGT CGTTGAGTCC TGGTGGTGT | 1920 |
| AATTGCAAGT TTGATGTTGC TGCACGTACA AGAACCAATG AGCAGGTTGT TAGAAGTCTA | 1980 |

| | |
|--|------|
| TATGTAATAT ATGAAGAAGG AGACAAACATA GTGGGTGTAC CGTCTGATRA TAGCGGTCTG | 2040 |
| CACGATTTGT CTGTGCTACA CCTAGACTCC TGTACAGATT ACAATATATA TGGTAGAACT | 2100 |
| GGTGTGGTA TTATTAGACG AACTAACAGT ACGCTACTTA GTGGCTTATA TTACACATCA | 2160 |
| CTATCAGGTG ATTTGTTAGG CTTTAAAAAT GTTAGTGATG GTGTCATTTA TTCTGTGACG | 2220 |
| CCATGTGATG TAAGCGCACA AGCGGC | 2246 |

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

| | |
|---|--|
| Met Ile Val Leu Val Thr Cys Leu Leu Leu Leu Cys Ser Tyr His Thr | |
| 1 5 10 15 | |
| Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln | |
| 20 25 30 | |
| Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe | |
| 35 40 45 | |
| Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val | |
| 50 55 60 | |
| Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe | |
| 65 70 75 80 | |
| Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser | |
| 85 90 95 | |
| Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu | |
| 100 105 110 | |
| Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln | |
| 115 120 125 | |
| Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg | |
| 130 135 140 | |
| His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys | |
| 145 150 155 160 | |
| Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn | |
| 165 170 175 | |
| Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala | |
| 180 185 190 | |
| Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe | |
| 195 200 205 | |
| Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu | |
| 210 215 220 | |
| Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr | |
| 225 230 235 240 | |

Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp
 245 250 255
 Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser
 260 265 270
 Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu
 275 280 285
 Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro
 290 295 300
 Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala
 305 310 315 320
 Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val
 325 330 335
 Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr
 340 345 350
 Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr
 355 360 365
 Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser
 370 375 380
 Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp
 385 390 395 400
 Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr
 405 410 415
 Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp
 420 425 430
 Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile
 435 440 445
 Xaa Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp
 450 455 460
 Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn
 465 470 475 480
 Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile
 485 490 495
 Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val
 500 505 510
 Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro
 515 520 525
 Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met
 530 535 540
 Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile
 545 550 555 560
 Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser
 565 570 575
 Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp
 580 585 590

133

Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala
 595 600 605

Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn
 610 615 620

Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala
 625 630 635 640

Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val
 645 650 655

Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly
 660 665 670

Val Pro Ser Asp Xaa Ser Gly Leu His Asp Leu Ser Val Leu His Leu
 675 680 685

Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile
 690 695 700

Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser
 705 710 715 720

Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile
 725 730 735

Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala
 740 745

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCG AGT ACG TCA AAC AAT GAT TGT AGA
 Ser Ser Thr Ser Asn Asn Asp Cys Arg
 1 5

27

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Ser Thr Ser Asn Asn Asp Cys Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAA AGT TTT AAA GAA GAA GGA ATT
Gln Ser Phe Lys Glu Glu Gly Ile
1 5

24

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gln Ser Phe Lys Glu Glu Gly Ile
1 5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCA ACT ACC ACT GCC TAT
Ala Thr Thr Thr Ala Tyr
1 5

18

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Ala Thr Thr Thr Ala Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGG GAT GAT GTG CAA CAA AGG CCA CTT TTA GAA CAT GGG TTA TTG. TGC
 Gly Asp Asp Val Gln Gln Arg Pro Leu Leu Glu His Gly Leu Leu Cys
 1 5 10 15

48

ATT ACT AAA AAT CGC AAT ATT GAC TAT AAC ACC TTC ACC AGC AAC CAG
 Ile Thr Lys Asn Arg Asn Ile Asp Tyr Asn Thr Phe Thr Ser Asn Gln
 20 25 30

96

TGG GAT TCC ATA TGT ACG GGT AAT GAC AGA AAA ATT CCT TTC TCT GTC
 Trp Asp Ser Ile Cys Thr Gly Asn Asp Arg Lys Ile Pro Phe Ser Val
 35 40 45

144

ATA CCC
Ile Pro
50

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gly Asp Asp Val Gln Gln Arg Pro Leu Leu Glu His Gly Leu Leu Cys
1 5 10 15

Ile Thr Lys Asn Arg Asn Ile Asp Tyr Asn Thr Phe Thr Ser Asn Gln
20 25 30

Trp Asp Ser Ile Cys Thr Gly Asn Asp Arg Lys Ile Pro Phe Ser Val
35 40 45

Ile Pro
• 50

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AAT ATT GAC TAT AAC ACC
Asn Ile Asp Tyr Asn Thr
1 5

18

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Asn Ile Asp Tyr Asn Thr
1 5

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTG TGC ATT ACT AAA AAT CGC AAT ATT GAC TAT AAC ACC TTC ACC AGC
Leu Cys Ile Thr Lys Asn Arg Asn Ile Asp Tyr Asn Thr Phe Thr Ser
1 5 10 15

48

AAC CAG TGG GAT TCC ATA
Asn Gln Trp Asp Ser Ile
20

66

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Leu Cys Ile Thr Lys Asn Arg Asn Ile Asp Tyr Asn Thr Phe Thr Ser
1 5 10 15

Asn Gln Trp Asp Ser Ile
20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAT CGC AAT ATT GAC TAT AAC ACC
Asn Arg Asn Ile Asp Tyr Asn Thr
1 5

24

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Asn Arg Asn Ile Asp Tyr Asn Thr
1 5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AAT TGG AAC ATC AAT AAT
Asn Trp Asn Ile Asn Asn
1 5

18

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asn Trp Asn Ile Asn Asn
1 5

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ATC TTT TTC GCA CAT ACC GCT ATC
Ile Phe Phe Ala His Thr Ala Ile
1 5

24

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile Phe Phe Ala His Thr Ala Ile
1 5

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

| | |
|---|-----|
| AAT GCT CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG CCT GTT | 48 |
| Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val | |
| 1 5 10 15 | |
| AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA CAA AGG | 96 |
| Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg | |
| 20 25 30 | |
| CCC CTT TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC CAT ATT | 144 |
| Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile | |
| 35 40 45 | |
| AAC TAT GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT ACG GGT | 192 |
| Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly | |
| 50 55 60 | |
| GCT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT GGA ACA | 240 |
| Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr | |
| 65 70 75 80 | |
| AAA ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT TAT ATT | 288 |
| Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile | |
| 85 90 95 | |
| AGT GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT AAC AAT | 336 |
| Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn | |
| 100 105 110 | |
| GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GA | 377 |
| Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp | |
| 115 120 125 | |

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

| | |
|---|--|
| Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val | |
| 1 5 10 15 | |
| Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg | |
| 20 25 30 | |
| Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile | |
| 35 40 45 | |
| Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly | |
| 50 55 60 | |
| Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr | |
| 65 70 75 80 | |
| Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile | |
| 85 90 95 | |

140

Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn
100 105 110

Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp
115 120 125